

Amendments to the Specification:

Please replace the first paragraph after the title (lines 3-5) with the following paragraph:

This application is the National Stage application of PCT/DK2004/000478 filed on July 2, 2004, which claims benefit to Danish Application No. PA 2003 01010 filed on July 3, 2003 and U.S. provisional Application No. 60/484,923, filed July 3, 2003 (now expired), which application(s) are incorporated herein by reference.

Please replace the third paragraph on page 17, lines 20-24, with the following paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein multiple sequence alignments and profile hidden Markov models used to identify conserved protein domains (Bateman *et al.*, 2002, Nucleic Acids Res. 30: 276-80; and searchable on [http://www. the internet at sanger.ac.uk/Software/Pfam/](http://www.theinternetatsanger.ac.uk/Software/Pfam/) and on NCBI at <http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi> .

Please replace the fourth paragraph on page 17, lines 26-30, with the following paragraph:

Protein domain prediction: sequences are analyzed by BLAST ([www.](http://www.ncbi.nlm.nih.gov/BLAST/) (ncbi.nlm.nih.gov/BLAST/) and PredictProtein ([www.](http://www.emblheidelberg.de/predictprotein/predictprotein) (emblheidelberg.de/predictprotein/predictprotein)). Signal peptides are predicted by SignalP v. 1.1 ([www.](http://www.cbs.dtu.dk/services/signalP/) (cbs.dtu.dk/services/signalP/)) and transmembrane regions are predicted by TMHMM v. 2.0 ([www.](http://www.cbs.dtu.dk/services/TMHMM/) (cbs.dtu.dk/services/TMHMM/)).

Please replace the paragraph on page 19, lines 19-31 through page 20, lines 1-4, with the following paragraph:

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: (~~www.ncbi.nlm.nih.gov/~~) (ncbi.nlm.nih.gov/)

Please replace the paragraph on page 53, lines 5-21, with the following:

The NFR5 Nod-factor binding proteins encoded by the *NFR5* alleles of *Lotus japonicus* ecotype GIFU (gene sequence: SEQ ID No: 7; protein sequence: SEQ ID No: 24 & 25), and *Lotus filicaulis* (gene sequence SEQ ID No: 30; protein sequence SEQ ID No: 31) have been compared, and found to show diversity in their primary structure. Using the sequence information available for the *Lotus NFR5* gene together with the pea SYM10 gene (Table 12), the alleles from different ecotypes or varieties of *Lotus*, pea and other legumes can now be identified, and used directly in breeding programs. By further way of example, the nucleic acid sequence of the *Phaseolus vulgaris NFR5* gene (SEQ ID No: 39) has facilitated the identification of a molecular marker for two different *NFR5* alleles in the *Phaseolus vulgaris* lines Bat93 and Jalo EEP558, that is based on a single nucleotide difference creating an Apol restriction site (RAATTY) in line Bat93, wherein R stands for A or G, Y for C or T. A partial sequence of the *NFR5* gene comprising the Apol site molecular marker identified in line Bat93 is shown in bold type:

CACAGGACATATTGAGTGAAAACAACTATGGTCAAA**ATTT**CACTGCCGC
AAGCAACCTTCCAGTTTTGATCCCAGTTACA (SEQ ID No: 55)

Please replace the paragraph on page 53, lines 22-25, with the following:

The absence of this Apol site in the comparable *NFR5* partial sequence of line Jalo EEP558 is shown in bold type:

CACAGGACATATTGAGTGAAAACAACTATGGTCAAA**ACTT**CACTGCCGC
AAGCAACCTTCCAGTTTTGATCCCAGTTACA (SEQ ID No: 56)

Please replace Table 1 on page 55 with the following:

Table 1

Alignment of Lotus, Glycine and Phaseolus NFR5 protein sequences

Lotus	1	MAVFF	1	GELEPLALT	2	LLFTNIAARE	3	EXISGPDPRC	4	PVNSPPSCET	50
Glycine	1	MAVFFPFLM	1	HEELICLYK	2	LLFTNIVAGS	3	QQNRTPRC	4	PHNSPPSCET	50
Phaseolus	1	MAVFFVELT	1	GEELVYVLM	2	FFTC	3	QQTCTNPRC	4	PENSPSCET	50
Lotus	5	YVTTAGEPH	6	ELSLTNED	7	PDSELEIA	8	ASNLDAHPR	9	LYPQCVLLV	100
Glycine	5	YVTTAGEPH	6	ELSLTNED	7	PDSELEIA	8	ASNLDAHPR	9	LYPQCVLLV	100
Phaseolus	5	YVTTAGEPH	6	ELSLTNED	7	PDSELEIA	8	ASNLDAHPR	9	LYPQCVLLV	100
Lotus	10	PTQCTGRRS	11	SANISYDGL	12	SDSYDVATT	13	LYSLTNWRI	14	YQASNPVRF	150
Glycine	10	PTQCTGRRS	11	SANISYDGL	12	SDSYDVATT	13	LYSLTNWRI	14	YQASNPVRF	150
Phaseolus	10	PTQCTGRRS	11	SANISYDGL	12	SDSYDVATT	13	LYSLTNWRI	14	YQASNPVRF	150
Lotus	15	YLLKRVVYV	16	PPLKCPKPK	17	NQLKMDIYV	18	TYVWKREN	19	VELVSLKCA	200
Glycine	15	YLLKRVVYV	16	PPLKCPKPK	17	NQLKMDIYV	18	TYVWKREN	19	VELVSLKCA	200
Phaseolus	15	YLLKRVVYV	16	PPLKCPKPK	17	NQLKMDIYV	18	TYVWKREN	19	VELVSLKCA	200
Lotus	20	SPADLTERR	21	YQGFYTAAN	22	LETLISYTV	23	PLQLGPRSD	24	AKNSIGLPI	250
Glycine	20	SPADLTERR	21	YQGFYTAAN	22	LETLISYTV	23	PLQLGPRSD	24	AKNSIGLPI	250
Phaseolus	20	SPADLTERR	21	YQGFYTAAN	22	LETLISYTV	23	PLQLGPRSD	24	AKNSIGLPI	250
Lotus	25	LGSLACITL	26	TVLTGVLTV	27	VYCHRRSLN	28	ESASSASTAD	29	KLLGTVGTV	300
Glycine	25	LGSLACITL	26	TVLTGVLTV	27	VYCHRRSLN	28	ESASSASTAD	29	KLLGTVGTV	300
Phaseolus	25	LGSLACITL	26	TVLTGVLTV	27	VYCHRRSLN	28	ESASSASTAD	29	KLLGTVGTV	300
Lotus	30	SKMVTYIKK	31	INSATYPLSD	32	KQVSGSYVK	33	AMIEGRVYV	34	KKIEGGRHS	350
Glycine	30	SKMVTYIKK	31	INSATYPLSD	32	KQVSGSYVK	33	AMIEGRVYV	34	KKIEGGRHS	350
Phaseolus	30	SKMVTYIKK	31	INSATYPLSD	32	KQVSGSYVK	33	AMIEGRVYV	34	KKIEGGRHS	350
Lotus	35	ELKILKQNH	36	GLVFLACTYS	37	SDYDNCFLV	38	YETAEAGSLA	39	SWLPAKSCD	400
Glycine	35	ELKILKQNH	36	GLVFLACTYS	37	SDYDNCFLV	38	YETAEAGSLA	39	SWLPAKSCD	400
Phaseolus	35	ELKILKQNH	36	GLVFLACTYS	37	SDYDNCFLV	38	YETAEAGSLA	39	SWLPAKSCD	400
Lotus	40	ETVNSLTN	41	SDRISLAVTV	42	AVSLQYNRS	43	TYPRITARR	44	TYNSILGRR	450
Glycine	40	ETVNSLTN	41	SDRISLAVTV	42	AVSLQYNRS	43	TYPRITARR	44	TYNSILGRR	450
Phaseolus	40	ETVNSLTN	41	SDRISLAVTV	42	AVSLQYNRS	43	TYPRITARR	44	TYNSILGRR	450
Lotus	45	PKAKIANPAP	46	ARTFTNPMF	47	KIDVPAPVY	48	LIELLTGRKA	49	MTTKNGRUV	500
Glycine	45	PKAKIANPAP	46	ARTFTNPMF	47	KIDVPAPVY	48	LIELLTGRKA	49	MTTKNGRUV	500
Phaseolus	45	PKAKIANPAP	46	ARTFTNPMF	47	KIDVPAPVY	48	LIELLTGRKA	49	MTTKNGRUV	500
Lotus	50	MLWCKNRYV	51	DIENREERT	52	KQKCPKLES	53	YPIIDYALH	54	ASLAVNCTAS	550
Glycine	50	MLWCKNRYV	51	DIENREERT	52	KQKCPKLES	53	YPIIDYALH	54	ASLAVNCTAS	550
Phaseolus	50	MLWCKNRYV	51	DIENREERT	52	KQKCPKLES	53	YPIIDYALH	54	ASLAVNCTAS	550
Lotus	55	KSLRPPMAH	56	IVLSLESLT	57	ESDPTLERS	58	ETPSGLDVA	59	SANFTETIT	600
Glycine	55	KSLRPPMAH	56	IVLSLESLT	57	ESDPTLERS	58	ETPSGLDVA	59	SANFTETIT	600
Phaseolus	55	KSLRPPMAH	56	IVLSLESLT	57	ESDPTLERS	58	ETPSGLDVA	59	SANFTETIT	600
Lotus	60	R	61	R	62	R	63	R	64	R	650
Glycine	60	R	61	R	62	R	63	R	64	R	650
Phaseolus	60	R	61	R	62	R	63	R	64	R	650

Please replace Table 3 on page 57 with the following:

Table 3

Alignment of *Lotus* and *Pisum* NFR1 protein sequences

<i>Pisum</i>	1	KKLKNGLLLF	7	KVSEHCYKGC	13	DLALASTYIM	19	50
<i>Pisum</i>	1	KKLKNGLLLF	7	KVSEHCYKGC	13	DLALASTYIM	19	50
<i>Lotus</i>	1	KKLKNGLLLF	7	KVSEHCYKGC	13	DLALASTYI	19	50
<i>Pisum</i>	5	TFMGGSLVTH	11	SPFVIVSYNR	17	STFRVNIFFP	23	100
<i>Pisum</i>	5	TFMGGSLVTH	11	SPFVIVSYNR	17	STFRVNIFFP	23	100
<i>Lotus</i>	5	TFMGGSLVTH	11	SPFVIVSYNR	17	STFRVNIFFP	23	100
<i>Pisum</i>	15	KVPEYTAAGK	21	QVYDLTANFY	27	KKPYEVNPPN	33	150
<i>Pisum</i>	15	KVPEYTAAGK	21	QVYDLTANFY	27	KKPYEVNPPN	33	150
<i>Lotus</i>	15	KVPEYTAAGK	21	QVYDLTANFY	27	KKPYEVNPPN	33	150
<i>Pisum</i>	15	VMSCGNSQI	21	SKDVEGITYY	27	PLKPGDTLFR	33	200
<i>Pisum</i>	15	VMSCGNSQI	21	SKDVEGITYY	27	PLKPGDTLFR	33	200
<i>Lotus</i>	15	VMSCGNSQI	21	SKDVEGITYY	27	PLKPGDTLFR	33	200
<i>Pisum</i>	25	PSKGGVYVF	31	PKRNNHREY	37	PLKPGDTLFR	43	250
<i>Pisum</i>	25	PSKGGVYVF	31	PKRNNHREY	37	PLKPGDTLFR	43	250
<i>Lotus</i>	25	PSKGGVYVF	31	PKRNNHREY	37	PLKPGDTLFR	43	250
<i>Pisum</i>	35	CITIKYPOK	41	EEETKLSQ	47	VSALSSAGS	53	300
<i>Pisum</i>	35	CITIKYPOK	41	EEETKLSQ	47	VSALSSAGS	53	300
<i>Lotus</i>	35	CITIKYPOK	41	EEETKLSQ	47	VSALSSAGS	53	300
<i>Pisum</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	350
<i>Pisum</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	350
<i>Lotus</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	350
<i>Pisum</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	400
<i>Pisum</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	400
<i>Lotus</i>	35	TAELTQINVA	41	KSTFPTQEL	47	ANATNPSLO	53	400
<i>Pisum</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	450
<i>Pisum</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	450
<i>Lotus</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	450
<i>Pisum</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	500
<i>Pisum</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	500
<i>Lotus</i>	45	QNLGGYLNR	51	GRKPLPWEK	57	QNLGGYLNR	63	500
<i>Pisum</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	550
<i>Pisum</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	550
<i>Lotus</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	550
<i>Pisum</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	600
<i>Pisum</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	600
<i>Lotus</i>	55	PKIDVYAFQV	61	VLVELLEK	67	AVLTGDSAV	73	600
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	650
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	650
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	650
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	700
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	700
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	700
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	750
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	750
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	750
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	800
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	800
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	800
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	850
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	850
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	850
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	900
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	900
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	900
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	950
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	950
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	950
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	1000
<i>Pisum</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	1000
<i>Lotus</i>	65	QNLGGYLNR	71	GRKPLPWEK	77	QNLGGYLNR	83	1000

Please replace Table 11 on page 64 with the following:

TABLE 11				
Marker	Genetic distance from NFR5 locus	<u>Molecular markers for NFR5 allele breeding in <i>Lotus</i></u>		SEQ ID NO:
		<i>Lotus</i> Ecotype	Microsatellite sequence	
TM0272	2.9 cM	MG-20	18xCT	
		Gifu	12xCT	
TM0257	1.0 cM	MG-20	10xAAG	
		Gifu	7xAAG	
LjT13i23Sfi		Gifu	TTTTGCTGCAGCAAGTCAGACTGTTAGAGGA	57
		Fili	TTTTGCTGCAACAAGTCGGACTGTTAGAGGA	58
TM0522	0 cM	MG-20	24xAT	
		Gifu	14xAT	
NFR5				
E32M54-12F	0.5 cM	MG-20	TTGGAAGTTCTTTTTATTAGGTTAATTTTA	59
		Fili	TTGGAAGTTCTTTTTA - - - GGTTAATTTTA	60
LJt01C03 Not	0.7 cM	Fili	CATTCCAGAAGAAAATAAGATATAATTATG	61
		MG-20	CATTCCAGAAGAAAATAAGATATAATTATG	61
		Gifu	CATTCCAGAAG - AAATAAGATATAATTATG	62
TM0168	2.2 cM	MG-20	19xAT	
		Gifu	15xAT	
TM0021	3.8 cM	MG-20	16xCT	
		Gifu	13xCT	

Please replace Table 12 on page 65 with the following:

Table 12

**Nucleotide sequence variation between the pea SYM10 alleles
of pea cultivars Frisson and Finale***

Frisson	CTTGCAATTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Finale	CTTGCAATTC	TTCACAATTT	CACAACAATG	GCTATCTTCT	TTCTTCCTTC
Frisson	TAGTTCTCAT	GCCCTTTTTT	TTGCACTCAT	GTTTTTTGTC	ACTAATATTT
Finale	TAGTTCTCAT	GCCCTTTTTT	TTGCACTCAT	GTTTTTTGTC	ACTAATATTT
Frisson	CAGCTCAACC	ATTACAACCT	AGTGAACAA	ACTTTTCATG	CCCGGTGGAT
Finale	CAGCTCAACC	ATTACAACCT	AGTGAACAA	ACTTTTCATG	CCCGGTGGAT
Frisson	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Finale	TCACCTCCTT	CATGTGAAAC	CTATGTGACA	TACTTTGCTC	GGTCTCCAAA
Frisson	CTTTTGGAGC	CTAACTAACA	TATCAGATAT	ATTTGATATG	AGTCCTTTAT
Finale	CTTTTGGAGC	CTAACTAACA	TATCAGATAT	ATTTGATATG	AGTCCTTTAT
Frisson	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Finale	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Frisson	GGCCAAGTCT	TACTCATACC	TGTAACCTGT	GGTTGCACTA	GAAATCGCTA
Finale	GGCCAAGTCT	TACTCATACC	TGTAACCTGT	GGTTGCACTA	GAAATCGCTA
Frisson	TTTCGGGAAT	TTCACGTACA	CAATCAAGCT	AGGTGACAAC	TATTTTCATG
Finale	TTTCGGGAAT	TTCACGTACA	CAATCAAGCT	AGGTGACAAC	TATTTTCATG
Frisson	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAAT
Finale	TTTCAACCAC	TTCATACCAG	AATCTTACAA	ATTATGTGGA	AATGGAAAAAT
Frisson	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Finale	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Frisson	TGTCCCTTTA	TTCTGCAAAT	GCCCCTCGAA	GAATCAGTTG	AGCAAAGGAA
Finale	TGTCCCTTTA	TTCTGCAAAT	GCCCCTCGAA	GAATCAGTTG	AGCAAAGGAA
Frisson	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCCGT
Finale	TAAAGCATCT	GATTACTTAT	GTGTGGCAGG	CTAATGACAA	TGTTACCCGT
Frisson	GTAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Finale	GTAAGTTCCA	AGTTTGGTGC	ATCACAAGTG	GATATGTTTA	CTGAAAACAA
Frisson	TCAAACTTC	ACTGCTTCAA	CCAACTTCC	GATTTTGATC	CCTGTGACAA
Finale	TCAAACTTC	ACTGCTTCAA	CCAACTTCC	GATTTTGATC	CCTGTGACAA
Frisson	AGTTACCGGT	AATTGATCAA	CCATCTTCAA	ATGGAAGAAA	AAACAGCACT
Finale	AGTTACCGGT	AATTGATCAA	CCATCTTCAA	ATGGAAGAAA	AAACAGCACT

Frissou	CAAAAACCTG CTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Finale	CAAAAACCTG CTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Frissou	TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Finale	TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Frissou	GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA
Finale	GATTGAATAG GAGTACTTCA TTGGCGGAGA CTGCGGATAA GTTACTTTCA
Frissou	GGTGTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Finale	GGTGTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Frissou	CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATCG
Finale	CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATCG
Frissou	TTTACAAGGC TAATATAGAT GGTAGAGTTF TAGCAGTGAA AAAATCAAG
Finale	TTTACAAGGC TAATATAGAT GGTAGAGTTF TAGCAGTGAA AAAATCAAG
Frissou	AAAGATGCTT CTGAGGAGCT GAAAATTG CAGAAGGTAA ATCATGGAAA
Finale	AAAGATGCTT CTGAGGAGCT GAAAATTG CAGAAGGTAA ATCATGGAAA
Frissou	TCTGTGAAA CTTATGGGTG TGTCTCCGA CAACGAGGA AACTGTTTCC
Finale	TCTGTGAAA CTTATGGGTG TGTCTCCGA CAACGAGGA AACTGTTTCC
Frissou	TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCCTCA
Finale	TTGTTTACGA GTATGCTGAA AATGGATCAC TTGATGAGTG GTTGTTCCTCA
Frissou	GAGTGTGCGA AAACCTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG
Finale	GAGTGTGCGA AAACCTCGAA CTCGGTGGTC TCGCTTACAT GGTCTCAGAG
Frissou	AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Finale	AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Frissou	ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Finale	ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Frissou	CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCOA TGGCCAGAAC
Finale	CTGGATTCAA ACTTTAAGGC CAAGATAGCG AATTTTTCOA TGGCCAGAAC
Frissou	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Finale	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Frissou	TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Finale	TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Frissou	GGCGAGGTGG TTATTCTGTG GAAGGATTTT TGGAGATTTT TTGATCTAGA
Finale	GGCGAGGTGG TTATTCTGTG GAAGGATTTT TGGAGATTTT TTGATCTAGA
Frissou	AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA
Finale	AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA

Frison	ATTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT
Finale	<u>ATTTTATCC TATTGATAAT GCTCTTAGTT TGGCTTCTTT GGCAGTGAAT</u>
Frison	TGTACTGCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT
Finale	<u>TGTACTGCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT</u>
Frison	TTGTCTTCT CTCTCAATC AATCATCATC TGAACCAATG TTAGAAAGAT
Finale	<u>TTGTCTTCT CTCTCAATC AATCATCATC TGAACCAATG TTAGAAAGAT</u>
Frison	CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTTGT TACTTCTATA
Finale	<u>CCTTGACATC TGGTTTAGAT GTTGAAGCTA CTCATGTTGT TACTTCTATA</u>
Frison	GTAGCTCCTT GATATTCATT CAAGTGAAGG TAACACTGAA TCAATGCTTC
Finale	<u>GTAGCTCCTT GATATTCATT CAAGTGAAGG TAACACTGAA TCAATGCTTC</u>
Frison	AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGCTGATT ATTGATTACA
Finale	<u>AGTTTCTTAT ATTCAAGATG GTTACTTTGT TTAGCTGATT ATTGATTACA</u>
Frison	TCTTTATGTG TGGAACTATA TGGTIATTTT AATTAAAGGA ATTCTCTAA
Finale	<u>TCTTTATGTG TGGAACTATA TGGTIATTTT AATTAAAGGA ATTCTCTAA</u>
Frison	ATTTCATTTT TCCATGTT SEQ ID NO: 13
Finale	<u>ATTTCATTTT TCCATGTT SEQ ID NO: 12</u>

* Nucleotide differences are shaded black and the coding region is underlined